5′ GGT GGC GAC GAC TCC TGG AGC CCG 3′	SEQ ID NO:6
5′ TTG ACA CCA GAC CAA CTG GTA ATG 3′	SEQ ID NO:7
5′ GAC CGC GAT GAT GTG GCT TTG AAG AAC 3′	SEQ ID NO:8
5′ GAT AGG ATC TTT AGC GAC AGC CGA 3′	SEQ ID NO:9
5′ ATG GCG GCC TCT GAG TCC TGG TGG 3′	SEQ ID NO:10
5′ CGG GCT GAA TGC AAT GGA GTG TGC 3′	SEQ ID NO:11
5′ GAC CCC CAT TTG TGT GAC 3′	SEQ ID NO:12
5′ CGA CGA CTC CTG GAG CCC G 3′	SEQ ID NO:13
5′ Biotin-TTG ACA CCA GAC CAA CTC GTA ATG 3′	SEQ ID NO:14
5′ AGC CGA CAG CGA TTT CTA GGA TAG 3′	SEQ ID NO:15
5′ GTT CTT CAA AGC CAC ATC ATC GCG GTC 3′	SEQ ID NO:16
5′ GCT TTC ATT ATC ACT GTC TCC CAG GGT G 3′	SEQ ID NO:17
5′ CAG ACG TTC TTC GCC GAG AGT CGT 3′	SEQ ID NO:18
5′ CAG ACG TTC TTC GCC GAG AGT CGT CGG 3′	SEQ ID NO:19
5′ CAT TTC GGG GAT TCG GGG GA 3′	SEQ ID NO:20
5′ GGG GGA CGG AAC CCG GCG CT 3′	SEQ ID NO:21
5′ CCC TCT ACA CTT ATC ATC TTC 3′	SEQ ID NO:22
5′ CTA TCC TAG AAA TCG CTG TCG GCT 3′	SEQ ID NO:23
5′ GTC ACT ACT GGA ATT CCC TTC TCC 3′	SEQ ID NO:24
5′ GGA GAA GGG AAT TCC AGT AGT GAC 3′	SEQ ID NO:25
5′ GGA AAT CGC TGT CGC CTA ACC 3′	SEQ ID NO:26
5′ GGT TAG GCG ACA GCG ATT TCC 3′	SEQ ID NO:27
5′ GGC CAC GCG TCG ACT AGT AC 3′	SEQ ID NO:28
5′ GTA ATG CAC ACTCCA TTG GC 3′	SEQ ID NO:29
5′ GTA ATG CAC ACT CCA TTG 3′	SEQ ID NO:30
5′ GCG CTC AGC TGG AAT TCC 3′	SEQ ID NO:31
5′ GGA ATT CCA GCT GAG CGC 3′	SEQ ID NO:32
5′ GTG GGA TCC CCA TGA CGA CCG CGT CCA CC 3′	SEQ ID NO:33
5′ GAC TCG AGT TAA GCC GAC AGC GAT TTC 3′	SEQ ID NO:34
5′ GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3′	SEQ ID NO:35
5′ CCC GCT CGA GTC AGG GTG ACC GAA AAA TCA G 3′	SEQ ID NO:36

Please replace the two paragraphs beginning at line 6 on page 16 and ending at line 13 of page 16 with the following rewritten paragraphs:

--**Fig. 1** shows the nucleic acid sequence (SEQ ID NO:1) of clone T16 isolated from T47D breast cancer cDNA library. Initiation and termination codons of the open reading frame are indicated by dark bars;

Fig. 2A shows a comparison of the nucleic acid sequences (upper sequence) (SEQ ID NO:2) of clone 4.7 isolated from a placenta cDNA library exhibiting normal human FTH, and the sequences (lower sequence) of clone T16 (SEQ ID NO:1) isolated from human breast cancer T47D cDNA library. Initiation and termination codons of the open reading frame are marked by dark boxes;--

Please replace the three paragraphs beginning at line 17 of page 16 and ending at line 25 of page 16 with the following rewritten paragraphs:

--**Fig. 3** shows a comparison of sequence homology between cDNA clone T16 (residues 463-671 of SEQ ID NO:1) and human mitochondrial cytochrone oxidase I DNA (SEQ ID NO:3);

Fig. 4 shows a comparison of nucleic acid sequences between placental cDNA obtained by PCR amplification using T16 specific primers (upper sequence) (residues 24-822 of SEQ ID NO:1) and T16 cDNA sequence obtained from the T16 cDNA clone (lower sequence) (SEQ ID NO:4). Identical nucleic acid sequences are indicated by a dotted line. Initiation and termination codons are indicated by a dark bar;

Fig. 5 shows the nucleic acid sequence and deduced amino acid sequence (SEQ ID NO:5) of the cDNA of OFF1;--

Please replace the two paragraphs beginning at line 4 of page 17 and ending at line 6 of page 17 with the following rewritten paragraphs:

--**Fig. 7** shows the sequence of clone T16 (SEQ ID NO:1). Primers used for PCR are indicated in the above sequence;

Fig. 8 shows the restriction enzyme map sequence of clone T16 (SEQ ID NO:1);--

Please replace Table 1 on page 19 with the following rewritten Table 1:

Table 1

List of Primers

Name	#MR	Sequence	SEQ ID NO:		
1060F	24	5′ GGT GGC GAC GAC TCC TGG AGC CCG 3′	6	75%	
1061R	24	5′ TTG ACA CCA GAC CAA CTG GTA ATG 3′	7	45.80%	
17F	27	5′ GAC CGC GAT GAT GTG GCT TTG AAG AAC 3′	8	52%	27618
X1.1F	24	5′ GAT AGG ATC TTT AGC GAC AGC CGA 3′	9	50%	24880
X.1.1R	24	5′ ATG GCG GCC TCT GAG TCC TGG TGG 3′	10	67%	
2.1F	24	5′ CGG GCT GAA TGC AAT GGA GTG TGC 3′	11	58%	
3.4F	18	5′ GAC CCC CAT TTG TGT GAC 3′	12	55.50%	
1060F/S	19	5′ CGA CGA CTC CTG GAG CCC G 3′	13	73.70%	
1061r/Bio	24	5′ Biotin-TTG ACA CCA GAC CAA CTC GTA ATG 3′	14	45.80%	
16X.1R	24	5′ AGC CGA CAG CGA TTT CTA GGA TAG 3′	15	50%	24879
17R	27	5′ GTT CTT CAA AGC CAC ATC ATC GCG GTC 3′	16	52%	27385
3′COD R	28	5′ GCT TTC ATT ATC ACT GTC TCC CAG GGT G 3′	17	50%	28313
5′ NCF	24	5′ CAG ACG TTC TTC GCC GAG AGT CGT 3′	18	58%	24870
4869	27	5′ CAG ACG TTC TTC GCC GAG AGT CGT CGG 3′	19	63%	
NFG	20	5′ CAT TTC GGG GAT TCG GGG GA 3′	20	60%	
NFGP-2	20	5′ GGG GGA CGG AAC CCG GCG CT 3′	21	80%	201880
767-F	21	5′ CCC TCT ACA CTT ATC ATC TTC 3′	22	43%	211616
16-F	24	5′ CTA TCC TAG AAA TCG CTG TCG GCT 3′	23	50%	241173
ECO-F	24	5′ GTC ACT ACT GGA ATT CCC TTC TCC 3′	24	50%	24960
ECO-R	24	5′ GGA GAA GGG AAT TCC AGT AGT GAC 3′	25	50%	24961
SPF	21	5′ GGA AAT CGC TGT CGC CTA ACC 3′	26	57%	211667
SPR	21	5′ GGT TAG GCG ACA GCG ATT TCC 3′	27	57%	211668
AUAP	20	5′ GGC CAC GCG TCG ACT AGT AC 3′	28	65%	202738
NC-F	20	5′ GTA ATG CAC ACTCCA TTG GC 3′	29	50%	203814
SNC-F	18	5′ GTA ATG CAC ACT CCA TTG 3′	30	44%	181897
BNC-F	18	5′ GCG CTC AGC TGG AAT TCC 3′	31	55.50%	181898
BNC-R	18	5′ GGA ATT CCA GCT GAG CGC 3′	32	61.10%	181905
pGEX-F	29	5′ GTG GGA TCC CCA TGA CGA CCG CGT CCA CC3′	33	67%	29391
pGEX-R1	27	5′ GAC TCG AGT TAA GCC GAC AGC GAT TTC 3′	34	51.85%	27578
pGEX-R2	29	5′ GAC TCG AGT CAG GGT GAC CGA AAA ATC AG 3′	35	51.70%	29396
pGEX-R3	31	5′ CCCGCTCGAGTCAGGGTGACCGAAAAATCAG 3′	36	58%	31277

Please replace the paragraph beginning at line 6 on page 27 with the following rewritten paragraph:

--The expression vector (pGEX-5X-1) used for gene fusion construction was the GST Gene Fusion System (Pharmacia). The OFF1 coding region (designated as *"FL"*, full-length) of about 0.5 kb was prepared by PCR with the following 5′ end primer:

5′ GT<u>GGGATCC</u>CCATGACGACCGCGTCCA (1-27 of SEQ ID NO:33), in order
BamHI

to add a BamHI site 1 base upstream from the start codon ATG and with the 3′ end primer

5′ CCCG <u>CTCGAG</u> TCA GGG TGA CCG AAA AAT CAG 3′ (SEQ ID NO:36) in
Xho1

order to add an Xho1 site after the stop codon TAA using the PCR kit (Perkin-Elmer/Centus).--

<u>IN THE DRAWINGS</u>

Attached hereto are copies of Figures 1, 2A, 5,, 7 and 8 with proposed revisions marked in red. Approval of these revisions is respectfully requested.

<u>IN THE SEQUENCE LISTING</u>

Please substitute the attached Sequence Listing, numbered as pages 1-8 for the Sequence Listing previously submitted.